

SEQUENCE LISTING

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Bouckaert, Julie

<120> Mutant Proteins, High Potency Inhibitory Antibodies, and FimCH Crystal Structure

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<170> PatentIn version 3.0

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 tgc ttg ctg gca ggt atc ctg atg ttc atg gca atg atg gtt gcc gga
 Cys Leu Leu Ala Gly Ile Leu Met Phe Met Ala Met Met Val Ala Gly
 20 25 30

 cgc gct gaa gcg gga gtg gcc tta ggt gcg act cgc gta att tat ccg
 Arg Ala Glu Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro
 35 40 45

 gca ggg caa aaa caa gtg caa ctt gcc gtg aca aat aat gat gaa aat
 Ala Gly Gln Lys Gln Val Gln Leu Ala Val Thr Asn Asn Asp Glu Asn
 50 55 60

 agt acc tat tta att caa tca tgg gtg gaa aat gcc gat ggt gta aag
 Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys
 65 70 75 80

 gat ggt cgt ttt atc gtg acg cct cct ctg ttt gcg atg aag gga aaa
 Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys
 85 90 95

 aaa gag aat acc tta cgt att ctt gat gca aca aat aac caa ttg cca
 Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro
 100 105 110

 cag gac cgg gaa agt tta ttc tgg atg aac gtt aaa gcg att ccg tca
 Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser
 115 120 125

atg gat aaa tca aaa ttg act gag aat acg cta cag ctc gca att atc Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile 130 135 140	432
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gat cag gcc gca gaa aaa tta aga ttt cgt cgt agc gcg aat tct ctg Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu 165 170 175	528
acg ctg att aac ccg aca ccc tat tac ctg acg gta aca gag ttg aat Thr Leu Ile Asn Pro Thr Pro Tyr Tyr Leu Thr Val Thr Glu Leu Asn 180 185 190	576
gcc gga acc cgg gtt ctt gaa aat gca ttg gtg cct cca atg ggc gaa Ala Gly Thr Arg Val Leu Glu Asn Ala Leu Val Pro Pro Met Gly Glu 195 200 205	624
acg acg gtt aaa ttg cct tct gat gca gga agc aat att act tac cga Ser Thr Val Lys Leu Pro Ser Asp Ala Gly Ser Asn Ile Thr Tyr Arg 210 215 220	672
aca ata aat gat tat ggc gca ctt acc ccc aaa atg acg ggc gta atg Thr Ile Asn Asp Tyr Gly Ala Leu Thr Pro Lys Met Thr Gly Val Met 225 230 235 240	720
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Ala Gly Gln Lys Gln Val Gln Leu Ala Val Thr Asn Asn Asp Glu Asn 50 55 60
Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys 65 70 75 80
Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys 85 90 95
Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro 100 105 110
Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser 115 120 125
Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile 130 135 140
Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro 145 150 155 160
Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu 165 170 175

Thr Leu Ile Asn Pro Thr Pro Tyr Tyr Leu Thr Val Thr Glu Leu Asn
 180 185 190
 Ala Gly Thr Arg Val Leu Glu Asn Ala Leu Val Pro Pro Met Gly Glu
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 Val Asn Ala Trp Ser Phe Ala Cys Lys Thr Ala Asn Gly Thr Ala Ile
 -5 -1 1 5 10
 cct att ggc ggt ggc agc gcc aat gtt tat gta aac ctt gcg ccc gtc 144
 Pro Ile Gly Gly Ser Ala Asn Val Tyr Val Asn Leu Ala Pro Val
 15 20 25
 gtg aat gtg ggg caa aac ctg gtc gtg gat ctt tcg acg caa atc ttt 192
 Val Asn Val Gly Gln Asn Leu Val Val Asp Leu Ser Thr Gln Ile Phe
 30 35 40
 tgc cat aac gat tat ccg gaa acc att aca gac tat gtc aca ctg caa 240
 Cys His Asn Asp Tyr Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln
 45 50 55
 cga ggc tcg gct tat ggc ggc gtg tta tct aat ttt tcc ggg acc gta 288
 Arg Gly Ser Ala Tyr Gly Gly Val Leu Ser Asn Phe Ser Gly Thr Val
 60 65 70 75
 aaa tat agt ggc agt agc tat cca ttt cct acc acc agc gaa acg ccg 336
 Lys Tyr Ser Gly Ser Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro
 80 85 90
 cgc gtt gtt tat aat tcg aga acg gat aag ccg tgg ccg gtg gcg ctt 384
 Arg Val Val Tyr Asn Ser Arg Thr Asp Lys Pro Trp Pro Val Ala Leu
 95 100 105
 tat ttg acg cct gtg agc agt gcg ggc ggg gtg gcg att aaa gct ggc 432
 Tyr Leu Thr Pro Val Ser Ser Ala Gly Gly Val Ala Ile Lys Ala Gly
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 Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser
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Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr	
160 165 170	
ctg ccg gac tac cct ggt tca gtg cca att cct ctt acc gtt tat tgt	624
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys	
175 180 185	
gcg aaa agc caa aac ctg ggg tat tac ctc tcc ggc aca acc gca gat	672
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp	
190 195 200	
gcg ggc aac tcg att ttc acc aat acc gcg tcg ttt tca cct gca cag	720
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln	
205 210 215	
ggc gtc ggc gta cag ttg acg cgc aac ggt acg att att cca gcg aat	768
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn	
220 225 230 235	
aac acg gta tcg tta gga gca gta ggg act tcg gcg gtg agt ctg gga	816
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly	
240 245 250	
tta acg gca aat tat gca cgt acc gga ggg cag gtg act gca ggg aat	864
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn	
255 260 265	
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 Val Asn Val Gly Gln Asn Leu Val Val Asp Leu Ser Thr Gln Ile Phe
 30 35 40
 Cys His Asn Asp Tyr Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln
 45 50 55
 Arg Gly Ser Ala Tyr Gly Gly Val Leu Ser Asn Phe Ser Gly Thr Val
 60 65 70 75
 Lys Tyr Ser Gly Ser Ser Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro
 80 85 90
 Arg Val Val Tyr Asn Ser Arg Thr Asp Lys Pro Trp Pro Val Ala Leu
 95 100 105
 Tyr Leu Thr Pro Val Ser Ser Ala Gly Gly Val Ala Ile Lys Ala Gly
 110 115 120

Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser
125 130 135
Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val
140 145 150 155
Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr
160 165 170
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys
175 180 185
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp
190 195 200
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln
205 210 215
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn
220 225 230 235
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly
240 245 250
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn
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270 275

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<212> DNA

<213> Artificial

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<223> Description of Artificial Sequence: Primer

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<210> 7

<211> 48

<212> DNA

<213> Artificial

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<223> Description of Artificial Sequence: Primer

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<210> 8

<211> 48

<212> DNA

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<223> Description of Artificial Sequence: Primer

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<212> DNA
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<210> 24
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<210> 28
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<210> 33
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<210> 44
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<210> 46
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<210> 47
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<400> 48
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<212> DNA
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